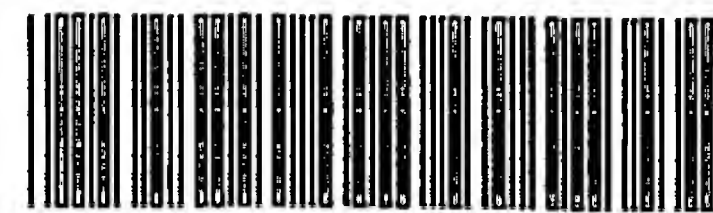


RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/593,841
Source: IFWP
Date Processed by STIC: 10/3/06

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IFWP

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DATE: 10/03/2006

PATENT APPLICATION: US/10/593,841

TIME: 08:45:28

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Output Set: N:\CRF4\10032006\J593841.raw

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3 <110> APPLICANT: University of Texas at San Antonio
4      Louisiana State University Health Sciences Center
5      Heidner, Hans Walter
6      Klimstra, William Brown
7      Ryman, Katherine Diana
9 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS COMPRISING PROTEIN L IMMUNOGLOBULIN
10     BINDING DOMAINS FOR CELL-SPECIFIC TARGETING
12 <130> FILE REFERENCE: 9237.21WO
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/593,841
C--> 14 <141> CURRENT FILING DATE: 2006-09-22
14 <160> NUMBER OF SEQ ID NOS: 27
16 <170> SOFTWARE: PatentIn version 3.2
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RAW SEQUENCE LISTING

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65	atg gct gca ctt gca ggt gca att gta gta aca ggt gga gta gga tct	348
66	Met Ala Ala Leu Ala Gly Ala Ile Val Val Thr Gly Gly Val Gly Ser	
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69	tac gca gct gat gaa cct att gat ctt gaa aaa ctt gaa gaa aaa agg	396
70	Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg	
71	20 25 30	
73	gat aaa gaa aat gta gga aat tta cca aaa ttc gat aat gaa gtt aaa	444
74	Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys	
75	35 40 45	
77	gat ggt tca gaa aat cca atg gct aaa tat cca gat ttc gat gat gaa	492
78	Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu	
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81	gcc agt aca aga ttt gaa aca gaa aac aat gaa ttt gaa gaa aaa aaa	540
82	Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys	
83	65 70 75 80	
85	gtt gtt tct gat aac ttt ttt gat caa tca gaa cat ccg ttt gta gaa	588
86	Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu	
87	85 90 95	
89	aat aaa gaa gaa aca cca gaa aca cca gaa act gat tca gaa gaa gaa	636
90	Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu	
91	100 105 110	
93	gta aca atc aaa gct aac cta atc ttt gca aat gga agc aca caa act	684
94	Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr	
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97	gca gaa ttc aaa gga aca ttt gaa aaa gca aca tca gaa gct tat gcg	732
98	Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala	
99	130 135 140	
101	tat gca gat act ttg aag aaa gac aat gga gaa tat act gta gat gtt	780
102	Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val	
103	145 150 155 160	
105	gca gat aaa ggt tat act tta aat att aaa ttt gct gga aaa gaa aaa	828
106	Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys	
107	165 170 175	
109	aca cca gaa gaa cca aaa gaa gaa gtt act att aaa gca aac tta atc	876
110	Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile	
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113	tat gca gat gga aaa aca caa aca gca gaa ttc aaa gga aca ttt gaa	924
114	Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu	
115	195 200 205	
117	gaa gca aca gca gaa gca tac aga tat gca gat gca tta aag aag gac	972
118	Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp	
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121	aat gga gaa tat aca gta gac gtt gca gat aaa ggt tat act tta aat	1020
122	Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn	
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130	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	
131				260					265					270			
133	gca	gaa	ttc	aaa	gga	aca	ttt	gaa	gaa	gca	aca	gca	gaa	gca	tac	aga	1164
134	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	
135			275					280					285				
137	tat	gct	gac	tta	tta	gca	aaa	gaa	aat	ggg	aaa	tat	aca	gta	gac	gtt	1212
138	Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu	Asn	Gly	Lys	Tyr	Thr	Val	Asp	Val	
139		290					295					300					
141	gca	gat	aaa	ggg	tat	act	tta	aat	att	aaa	ttt	gct	gga	aaa	gaa	aaa	1260
142	Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	
143	305					310					315					320	
145	aca	cca	gaa	gaa	cca	aaa	gaa	gaa	gtt	act	att	aaa	gca	aac	tta	atc	1308
146	Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	
147				325					330					335			
149	tat	gca	gat	gga	aaa	act	caa	aca	gca	gag	ttc	aaa	gga	aca	ttt	gca	1356
150	Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Ala	
151			340						345				350				
153	gaa	gca	aca	gca	gaa	gca	tac	aga	tac	gct	gac	tta	tta	gca	aaa	gaa	1404
154	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu	
155			355					360				365					
157	aat	ggg	aaa	tat	aca	gca	gac	tta	gaa	gat	ggg	gga	tac	act	att	aat	1452
158	Asn	Gly	Lys	Tyr	Thr	Ala	Asp	Leu	Glu	Asp	Gly	Gly	Tyr	Thr	Ile	Asn	
159		370					375					380					
161	att	aga	ttt	gca	ggg	aag	aaa	gtt	gac	gaa	aaa	cca	gaa	gaa	aaa	gaa	1500
162	Ile	Arg	Phe	Ala	Gly	Lys	Lys	Val	Asp	Glu	Lys	Pro	Glu	Glu	Lys	Glu	
163	385					390					395					400	
165	caa	gta	aca	att	aaa	gaa	aat	ata	tat	ttt	gaa	gat	gga	aca	gta	caa	1548
166	Gln	Val	Thr	Ile	Lys	Glu	Asn	Ile	Tyr	Phe	Glu	Asp	Gly	Thr	Val	Gln	
167				405					410				415				
169	act	gca	aca	ttt	aaa	gga	aca	ttt	gca	gaa	gcg	aca	gca	gaa	gca	tac	1596
170	Thr	Ala	Thr	Phe	Lys	Gly	Thr	Phe	Ala	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	
171			420						425				430				
173	aga	tat	gca	gat	ttg	tta	tca	aaa	gaa	cat	ggg	aaa	tac	aca	gca	gac	1644
174	Arg	Tyr	Ala	Asp	Leu	Leu	Ser	Lys	Glu	His	Gly	Lys	Tyr	Thr	Ala	Asp	
175			435					440				445					
177	ttg	gaa	gat	ggg	gga	tac	act	atc	aac	att	aga	ttt	gct	gga	aaa	gaa	1692
178	Leu	Glu	Asp	Gly	Gly	Tyr	Thr	Ile	Asn	Ile	Arg	Phe	Ala	Gly	Lys	Glu	
179		450					455					460					
181	gaa	cca	gaa	gaa	aca	cca	gaa	aaa	cca	gaa	gta	caa	gac	gga	tat	gca	1740
182	Glu	Pro	Glu	Glu	Thr	Pro	Glu	Lys	Pro	Glu	Val	Gln	Asp	Gly	Tyr	Ala	
183	465					470					475					480	
185	tca	tac	gaa	gaa	gct	gaa	gca	gca	gct	aaa	gaa	gct	ttg	aaa	aat	gat	1788
186	Ser	Tyr	Glu	Glu	Ala	Glu	Ala	Ala	Ala	Lys	Glu	Ala	Leu	Lys	Asn	Asp	
187				485					490				495				
189	gat	gta	aat	aaa	tca	tat	act	att	aga	caa	ggg	gca	gat	gga	aga	tat	1836
190	Asp	Val	Asn	Lys	Ser	Tyr	Thr	Ile	Arg	Gln	Gly	Ala	Asp	Gly	Arg	Tyr	

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194 Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Glu Glu Lys Pro Glu Ala
195          515          520          525
197 caa aat gga tat gca aca tac gaa gaa gca gaa gca gca gct aag aaa 1932
198 Gln Asn Gly Tyr Ala Thr Tyr Glu Glu Ala Glu Ala Ala Ala Lys Lys
199          530          535          540
201 gct ttg gaa aat gat cca atc aat aaa tct tac agc ata aga caa ggt 1980
202 Ala Leu Glu Asn Asp Pro Ile Asn Lys Ser Tyr Ser Ile Arg Gln Gly
203 545          550          555          560
205 gca gat gga aga tac tac tat gta tta tca cca gta gaa gct gaa act 2028
206 Ala Asp Gly Arg Tyr Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Thr
207          565          570          575
209 cct gaa aaa cca gta gaa cca tca gaa cca tca aca cca gat gta cca 2076
210 Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro
211          580          585          590
213 tca aac cca tca aat cca tca aca cca gat gtt cca tca act cct gat 2124
214 Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp
215          595          600          605
217 gta cca tca aat cct tca act cca gaa gtt cct tca aac cca tca act 2172
218 Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr
219          610          615          620
221 cct ggt aat gaa gaa aaa cct ggt aac gaa caa aaa cct ggt aac gaa 2220
222 Pro Gly Asn Glu Glu Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu
223 625          630          635          640
225 caa aaa cct ggt aac gaa caa aaa cct ggt aat gaa caa aaa cct ggt 2268
226 Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly
227          645          650          655
229 aat gaa caa aaa cca gac caa cct tca aaa cca gaa aaa gaa gaa aat 2316
230 Asn Glu Gln Lys Pro Asp Gln Pro Ser Lys Pro Glu Lys Glu Glu Asn
231          660          665          670
233 ggt aag ggt gga gta gat tct cca aag aaa aaa gaa aaa gct gca tta 2364
234 Gly Lys Gly Gly Val Asp Ser Pro Lys Lys Lys Glu Lys Ala Ala Leu
235          675          680          685
237 cca aaa gct ggt agc gaa gct gaa atc tta aca tta gca gca gct tca 2412
238 Pro Lys Ala Gly Ser Glu Ala Glu Ile Leu Thr Leu Ala Ala Ala Ser
239          690          695          700
241 tta tca agc gtt gca ggt gct ttc att tca ctt aaa aaa cgt aaa taa 2460
242 Leu Ser Ser Val Ala Gly Ala Phe Ile Ser Leu Lys Lys Arg Lys
243 705          710          715
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270          35          40          45
273 Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
274          50          55          60
277 Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
278 65          70          75          80
281 Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
282          85          90          95
285 Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu
286          100         105         110
289 Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr
290          115         120         125
293 Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala
294          130         135         140
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298 145         150         155         160
301 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
302          165         170         175
305 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
306          180         185         190
309 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu
310          195         200         205
313 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp
314          210         215         220
317 Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn
318 225         230         235         240
321 Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu
322          245         250         255
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326          260         265         270
329 Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg
330          275         280         285
333 Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val
334          290         295         300
337 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
338 305         310         315         320
341 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
342          325         330         335
345 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala
346          340         345         350
349 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu
350          355         360         365
353 Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn
354          370         375         380
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VERIFICATION SUMMARY

DATE: 10/03/2006

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TIME: 08:45:29

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date